SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 and which shares at least 50% identity therewith, said variant being capable of affecting one or more physical characteristics of a plant into which the nucleic acid is introduced, the physical characteristics being selected from vernalization response, flowering time, leaf size and/or shape or shade avoidance response, said isolated nucleic acid optionally comprising a sequence having promoter and/or regulatory function.

B7 Cont.d

61. A nucleic acid according to claim 60 wherein the variant is an allelic variant of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 or is a nucleic acid degenerative equivalent thereof.

62. A nucleic acid according to claim 60 wherein the variant sequence is a VRN2 sequence obtainable from a plant species other than Arabidopsis thaliana.

63. An isolated nucleic acid sequence according to claim 60, which is a derivative of said sequence by way of one or more of addition, insertion, deletion or substitution of a said nucleotide sequence, and wherein said derivative shares at least 50% homology with a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 and wherein the derivative sequence is either capable of affecting one or more physical characteristics of a plant into which the nucleic acid is introduced, the physical characteristics being selected from vernalization response, flowering time, leaf size and/or shape or shade avoidance response or has promoter and/or regulatory function.

64. An isolated nucleic acid which comprises a sequence

selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 which is a fragment of a sequence and either is capable of affecting one or more physical characteristics of a plant into which the nucleic acid is introduced, the physical characteristics being selected from vernalization response, flowering time, leaf size and/or shape or shade avoidance response or has promoter and/or regulatory function.

B7 cont'd

65. An isolated nucleic acid which comprises a sequence which is the complement of a sequence of claim 60.

66. An isolated nucleic acid for use as a probe or primer which comprises a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said nucleic acid is 15 to 40 nucleotides in length.

67. An isolated nucleic acid for use as a probe or primer which comprises a sequence that is partly, substantially or completely conserved between two or more of the VRN2 nucleotide sequences selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 or the complements thereof, wherein said nucleic acid is 15 to 40 nucleotides in length said nucleic acid optionally comprising a sequence having promoter and or regulatory function.

68. A nucleic acid according to claim 67 which is 19 to 28 nucleotides in length.

69. A pair of primers each comprising a nucleic acid according to claim 67.

70. A pair of primers according to claim 69 which is selected from:

VRN2-AP and VRN2-AJ;
VRN2-AO and VRN2-AS; and
VRN2-AI and VRN2-AJ.

71. A process for producing a nucleic acid which is a derivative according to claim 63 which process comprises the step of modifying a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7.

72. A method for identifying or cloning a nucleic acid according to claim 60 in a database search, which method comprises using a nucleotide sequence of a probe or primer comprising a sequence that is partly, substantially or completely conserved between two or more of the VRN2 nucleotide sequences selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 or the complements thereof, wherein said probe or primer is 15 to 40 nucleotides in length.

73. A method for identifying or cloning a nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said nucleic acid is 15 to 40 nucleotides in length or a pair of primers selected from the group consisting of VRN2-AP and VRN2-AJ; VRN2-AO and VRN2-AS; and
VRN2-AI and VRN2-AJ.

74. A method for determining the presence of a nucleic acid according claim 60 within the genetic make-up of a plant, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said nucleic acid is 15 to 40 nucleotides in length, or a pair of primers selected from the group consisting of VRN2-AP and VRN2-AJ; VRN2-AO and VRN2-AS; and
VRN2-AI and VRN2-AJ.

B7 cont'd

75. A method according to claim 73, which comprises the steps of:

(a) providing a preparation of nucleic acid from a plant cell;

(b) providing a nucleic acid molecule which is a probe, said probe comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said probe is 15 to 40 nucleotides in length;

(c) contacting nucleic acid in said preparation with said probe under conditions for hybridisation; and

(d) identifying a nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7, if present by its hybridisation with said nucleic acid probe.

76. A method according to claim 73, which method comprises the steps of:

(a) providing a preparation of nucleic acid from a plant cell;

(b) providing a pair of nucleic acid molecule primers suitable for PCR, at least one of said primers being a primer

which comprises a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said nucleic acid is 15 to 40 nucleotides in length;

(c) contacting nucleic acid in said preparation with said primers under conditions for performance of PCR;

(d) performing PCR and determining the presence or absence of an amplified PCR product.

B2 Cont'd

77. A method according to claim 76 wherein the pair of nucleic acid molecule primers are VRN2-AP and VRN2-AJ;
VRN2-AO and VRN2-AS; and
VRN2-AI and VRN2-AJ.

78. A method of selecting a plant having a desired allele of the VRN2 gene, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said nucleic acid is 15 to 40 nucleotides in length, or a pair of primers selected from the group consisting of
VRN2-AP and VRN2-AJ;
VRN2-AO and VRN2-AS; and
VRN2-AI and VRN2-AJ.

79. A recombinant vector which comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 or a sequence degeneratively equivalent thereto.

80. A vector according to claim 79 wherein the nucleic acid comprised in the vector is capable of regulating one or more genes involved in the transition from vegetative to reproductive growth and/or capable of regulating one or more genes involved in the determination of leaf size and/or shape.

81. A vector according to claim 80 wherein the nucleic acid is operably linked to a promoter for transcription in a host cell, wherein the promoter is optionally an inducible promoter.

82. A vector according to claim 81 wherein the promoter is a constitutive promoter.

83. A vector according to any one of claims 79 which is a plant vector.

84. A method which comprises the step of introducing a vector according to claim 79 into a host cell such as to transform the host cell.

85. A host cell which is transformed with a heterologous nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 and sequences degeneratively equivalent thereto.

86. A host cell according to claim 85 which is a plant cell, optionally present in a plant.

87. A method for producing a transgenic plant, which method comprises the steps of:

(a) performing a method according to claim 84; and

(b) regenerating a plant from the transformed host cell.

88. A transgenic plant which is obtainable by the method of claim 87, or which is a clone, or selfed or hybrid progeny or other descendant of said transgenic plant, which in each case includes the plant cell transformed with a heterologous nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 and sequences degeneratively equivalent thereto.

89. A plant according to claim 88 which is agricultural or horticultural plant.

90. A plant according to claim 89 selected from the list consisting of: rice, maize, wheat, barley, oats, rye, oil seed rape, sugar beet, sunflower, soybean, sorghum, lettuce, endive, cabbage, broccoli, cauliflower, carnation, geranium, tobacco, cotton, canola, tomato, mango, peach, apple, pear, strawberry, banana, melon, carrot, onion, pea, celery.

B2 cont'd

91. A plant according to claim 90 which is selected from tobacco, oil seed rape, rice and wheat.

92. A part or propagule from a plant which is a clone, or selfed or hybrid progeny or other descendant of said transgenic plant, which in each case includes the plant cell transformed with a heterologous nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 and sequences degeneratively equivalent thereto.

93. An isolated polypeptide which is encoded by a nucleotide sequence according to claim 1.

94. A polypeptide according to claim 93 which comprises an amino acid sequence which consists of the sequence of SEQ ID Nos. 2, 5 or 8.

95. A polypeptide which is a fragment of a polypeptide of claim 94, having at least nine contiguous amino acids.

96. An isolated polypeptide which consists of the sequence of SEQ ID Nos. 2, 5 or 8.

97. An isolated polypeptide which is a fragment of a polypeptide according to claim 96 and which comprises at least 9 contiguous amino acids of that polypeptide.

98. A fragment according to claim 97 which comprises amino acids 90 to 111 (zinc finger motif), amino acids 63 to 132 (amino terminal region), amino acids 263 to 366 (carboxy terminus) or amino acids 263 to 328 (activation domain).

99. A polypeptide according to claim 93 which is capable of affecting one or more physical characteristics of a plant expressing said peptide, the physical characteristics being selected from vernalization response, flowering time, leaf size and/or shape or shade avoidance response.

B2 cont'd

100. An isolated nucleic acid which encodes a fragment according to claim 97.

101. An isolated nucleic acid which is the complement of the nucleic acid of claim 100.

102. A method of making the polypeptide of a sequence selected from the group consisting of SEQ ID NO: 2, 5, or 8, which method comprises the step of causing or allowing expression from a nucleic acid encoding SEQ ID NOS 2, 5, or 8.

103. An antibody which has specific binding affinity for a polypeptide according to claim 93.

104. A polypeptide which comprises the antigen-binding site of the antibody of claim 103.

105. A method for affecting a physical characteristic of a plant selected from vernalization response, flowering time, leaf size and/or shape or shade avoidance response, which method comprises either the step of:

(i) causing or allowing transcription from a nucleic acid which comprises a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 or a fragment of said sequence